GENETIC POLYMORPHISMS OF ESTROGEN RECEPTOR ALPHA ASSOCIATED WITH FAVORABLE HDL CHOLESTEROL RESPONSE TO HORMONE REPLACEMENT THERAPY

[0001] Statement of Support

[0002] This invention was made with government support under grant number HL46488 from the National Institutes of Health. The United States government may have certain rights to this invention.

[0003] Cross Reference to Related Applications

[0004] This application claims the benefit of United States Provisional Application 60/270,700, filed on February 22, 2001, the disclosure of which is incorporated herein by reference in its entirety.

[0005] Field of the Invention

[0006] The present invention concerns methods for beneficially increasing HDL cholesterol levels in subjects.

[0007] Background of the Invention

[0008] Endogenous estrogen prior to menopause, and exogenous estrogen use after menopause, results in elevations of HDL cholesterol in women. This effect is often cited as a potential explanation for lower rates of heart disease in premenopausal women and postmenopausal women taking estrogen replacement. Sullivan et al., *Ann Intern Med* 1988; 108:358-363; and Gerhard et al., *Circulation* 1995; 92:5-8. However, there is considerable variability among women in terms of premenopausal HDL levels and changes in HDL in response to postmenopausal estrogen replacement. A significant portion of this variability has been attributed to genetic factors. Mahaney et al., *Arterioscler Thromb Vasc Biol* 1995; 15:1730-1739; and Austin et al., *Am J Hum Genet* 1998; 62:406-419. Allelic variants of the estrogen receptor alpha (ER-α) gene that alter the expression, function, or stability of the expressed receptor protein may account for some of this variation. Functionally significant mutations in other steroid receptor genes including receptors for androgens, mineralocorticoids, vitamin D, and glucocorticoids have already been described. Being able to identify women who are likely to have a more favorable lipid response to estrogen would

be useful for patients and their physicians as they weigh the risks and benefits of estrogen replacement therapy.

[0009] **Summary of the Invention**

[0010] A first aspect of the present invention is, accordingly, a method of screening a subject for increased likelihood of having a favorable response to estrogen replacement therapy., particularly with respect to cardiovascular health (*e.g.,* improved future cardiovascular health as compared to that found in the same patient without estrogen replacement therapy; a decreased probability of), heart disease (*e.g.,* a decreased , heart disease (*i.e.,* high density lipoprotein (HDL) level. The method comprises detecting the presence of at least one estrogen receptor alpha polymorphism in the subject, the presence of the estrogen receptor alpha polymorphism indicating the subject is more likely to have a favorable response to estrogen replacement therapy.

[0011] Estrogen receptor alpha polymorphisms of interest herein (that is, polymorphisms the detection of which would indicate an increased likelihood of a favorable response to estrogen replacement therapy, are, in general, the rare form of estrogen receptor alpha polymorphisms, and in particular include the rare form of polymorphisms found in the first intron of the estrogen receptor alpha gene. Examples of suitable polymorphisms include the IVS1-1415 polymorphism (also called the C/T Intron 1 polymorphism, at a position 1415 base pairs before the beginning of exon 2), the IVS1-1505 polymorphism (also called the A/G Intron 1 polymorphism, at a position 1505 base pairs before the beginning of exon 2), the IVS1-401 polymorphism (also called the PvuII polymorphism (a C/T SNP)), and the IVS1-354 polymorphism (also called the XbaI polymorphism (an A/G SNP)). The detection of the polymorphism can include detecting whether or not the subject is heterozygous or homozygous for the polymorphism, and the detection step can also include detecting two or more different such polymorphisms in the subject.

[0012] A second aspect of the present invention is a method for beneficially affecting cardiovascular health, decreasing the risk of heart disease, and/or increasing HDL levels in a subject (*e.g.* beneficially altering the LDL/HDL ratio), the method comprising: *(a)* determining the presence of at least one estrogen receptor alpha polymorphism in said subject; and then, if said estrogen receptor alpha polymorphism is present, *(b)* administering estrogen replacement therapy to said subject in an amount effective to beneficially affect cardiovascular health, decrease the risk of heart disease, and/orincrease HDL levels in said subject. Polymorphisms of interest are as discussed aboveabove.

[0013] A further aspect of the present invention is a method of treating a subject for depressed HDL levels (i.e., depressed in absolute levels or depressed relative to LDL levels), said method comprising the steps of: selecting a subject that carries at least one estrogen receptor alpha polymorphism, and administering estrogen replacement therapy to said subject in an amount effective to increase HDL levels (*e.g.,* beneficially alter the LDL/HDL ratio) in said subject. Polymorphisms of interest are as discussed above.

[0014] A further aspect of the present invention is the use of one or more estrogen replacement therapy active agents for the preparation of a medicament for carrying out a method as described above.

[0015] A further aspect of the present invention is the use of a means of detecting an estrogen receptor alpha polymorphism of interest in determining if a subject is suitable for treatment with hormone replacement therapy for beneficially affecting cardiovascular health, decreasing risk of heart disease, and/or raising HDL levels in that subject. Polymorphisms of interest are the same as discussed above.

[0016] Still further aspects of the present invention include kits, reagents such as oligonucleotide probes, restriction enzymes and other such means for carrying out methods as described above, the use of such reagents for the preparation of kits or diagnostic reagents for carrying out the methods described above, the use of the estrogen receptor polymorphisms described above in structuring clinical trials of estrogen replacement therapy active agents for beneficial efficacy as discussed above, and the use of the estrogen receptor polymorphisms as targets for rational drug design.

[0017] The foregoing and other objects and aspects of the present invention are explained in greater detail in the drawings herein and the specification set forth below.

~~[0018]~~ Brief Description of the Drawings

~~[0019]~~ **Figure 1.** The human estrogen receptor-α (*ER*-α) gene. Numbered boxes indicate exons. Vertical arrows indicate single nucleotide polymorphisms (SNPs) and the TA microsatellite repeat (above = previously recognized variants, below = new variants). Portions resequenced for novel SNP detection are indicated by dotted lines. Intronic regions (solid black lines) are not drawn to scale. Small numbers under each intron indicate the estimated size of the intron expressed as kilobase pairs.

~~[0020]~~ **Figure 2.** Baseline and follow-up high-density lipoprotein cholesterol (HDL-C) among women in the ERA trial by active arms vs placebo and *ER*-α IVS1-401 genotype

adjusted for age, race, body mass index, diabetes, smoking, exercise, and alcohol intake. P value is for the HRT by genotype interaction. HRT = hormone replacement therapy.

~~[0021]~~ **Figure 3A-D.** Baseline and follow-up levels of HDL_2 (panel A), HDL_3 (panel B), Apo A-I (panel C), and sex hormone-binding globulin (SHBG) (panel D) in ERA women on active therapy stratified by IVS1-401 genotype. Results from women on placebo not shown. Results are expressed as group means with error bars indicating standard errors. P values are for the treatment by genotype interaction after adjusting for potential confounders.

[0022] Detailed Description of the Preferred Embodiments

[0023] As noted above, the method of the present invention is concerned with, among other things, determining whether a subject will have a favorable response to estrogen replacement therapy, for example with respect to cardiovascular health, heart disease, and/or HDL levels. A favorable response with respect to cardiovascular health may be, for example, improved future cardiovascular health as compared to that expected in the same patient without estrogen replacement therapy; lack of an unduly deleterious effect on cardiovascular health as compared to patients without the detected polymorphism, etc. A favorable response with respect to heart disease may be, for example, a decreased risk of heart disease as compared to that expected in the same patient without estrogen replacement therapy, lack of an unduly deleterious increase in risk of heart disease as compared to patients without the detected polymorphism, etc. A favorable response with respect to HDL levels may be, for example, an increase in HDL levels as compared to that expected in the same patient without estrogen replacement therapy, lack of an unduly deleterious decrease in HDL levels as compared to that found in patients without the detected polymorphism, etc. By "HDL levels" is meant both absolute HDL levels and relative HDL levels (*e.g.*, an improved ratio of HDL to LDL).

[0024] Subjects for screening and/or treatment with the present invention are, in general, human subjects, and are preferably female subjects. The subject may be of any race and any age, including juvenile, adolescent, and adult, with adult subjects currently preferred, and post-menopausal, post-hysterectomy or other low estrogen subjects particularly preferred. The subject may also be a pre-menopausal female afflicted with low HDL levels. It will be appreciated by those skilled in the art that, while the present methods are useful for screening subjects to provide an initial indication of the suitability of a patient for a particular patient, this information will typically be considered by a clinician or medical practitioner in

light of other factors and experience in reaching a final judgment as to the treatment which any given subject should receive.

[0025] An increase of high density lipoprotein (HDL) levels in a subject herein is meant both *(i)* an increase in absolute HDL levels and *(ii)* a relative increase in HDL levels as compared to low density lipoprotein (LDL) levels. The latter may be achieved by a decrease in absolute LDL levels, even where absolute HDL levels are substantially the same (or even decreasing, albeit to a lesser extent than a decrease in HDL levels).

[0026] 1. <u>Polymorphism detection.</u>

[0027] In general, the step of detecting the polymorphism of interest may be carried out by collecting a biological sample containing DNA from the subject, and then determining the presence or absence of DNA containing the polymorphism of interest in the biological sample. Any biological sample which contains the DNA of that subject may be employed, including tissue samples and blood samples, with blood cells being a particularly convenient source. The nucleotide sequence of human estrogen receptor alpha is known and suitable probes, restriction enzyme digestion techniques, or other means of detecting the polymorphism may be implemented based on this known sequence in accordance with standard techniques. *See, e.g.,* U.S. Patent Nos. 6,027,896 and 5,767,248 to A. Roses et al. The human estrogen receptor alpha is known. The cDNA sequence is given at GENBANK accession number X03635 (**SEQ ID NO: 1**), the sequence of exon 1 is given at GENBANK accession number X03635, and the sequence of exon 2 is given at GENBANK accession number AF123494 (**SEQ ID NO: 3**). The estrogen receptor alpha gene has been mapped to q25.1-ter of chromosome 6. The gene spans a region 296 kilobases (kb) in size, and comprises of 8 exons and their intervening introns. The gene sequence is available in the literature or from public databases such as GenBank. See GenBank accession no. NT_023451.8, nucleotides c5,431,852 - 5,136,132, the disclosure of which is incorporated herein in its entirety.

[0028] The polymorphisms described herein can be detected in accordance with known techniques based upon the known sequence information of the human estrogen receptor alpha and the information provided herein. Novel genes described herein can be isolated from human sources based upon the information provided herein or produced by other means such as site-directed mutagenesis of known or available nucleic acids.

[0029] The least common allele or rare allele for the intron 1 polymorphisms described herein are preferred: That is, they provide a favorable indication of response to

estrogen replacement therapy with respect to HDL levels. The IVS1-401 (or PvuII) and IVS1-354 (or XbaI) polymorphisms are known. For IVS1-401/PvuII the rare allele is C. For IVS1-354/XbaI the rare allele is G.

[0030] The IVS1-1505 (or A/G intron 1) polymorphism (which is at a location 1505 base pairs before the start of exon 2) is newly described herein. G is the rare allele and hence preferred.

[0031] The IVS1-1415 (or C/T intron 1) polymorphism (which is at a location 1415 base pairs before the start of exon 2) is newly described herein. T is the rare allele and hence preferred.

[0032] Determining the presence or absence of DNA containing a polymorphism of interest may be carried out with an oligonucleotide probe labelled with a suitable detectable group, or by means of an amplification reaction such as a polymerase chain reaction or ligase chain reaction (the product of which amplification reaction may then be detected with a labelled oligonucleotide probe or a number of other techniques). Further, the detecting step may include the step of detecting whether the subject is heterozygous or homozygous for the polymorphism of interest. Numerous different oligonucleotide probe assay formats are known which may be employed to carry out the present invention. See, e.g., U.S. Pat. No. 4,302,204 to Wahl et al.; U.S. Pat. No. 4,358,535 to Falkow et al.; U.S. Pat. No. 4,563,419 to Ranki et al.; and U.S. Pat. No. 4,994,373 to Stavrianopoulos et al. (applicants specifically intend that the disclosures of all U.S. Patent references cited herein be incorporated herein by reference).

[0033] Amplification of a selected, or target, nucleic acid sequence may be carried out by any suitable means. See generally D. Kwoh and T. Kwoh, Am. Biotechnol. Lab. 8, 14-25 (1990). Examples of suitable amplification techniques include, but are not limited to, polymerase chain reaction, ligase chain reaction, strand displacement amplification (see generally G. Walker et al., Proc. Natl. Acad. Sci. USA 89, 392-396 (1992); G. Walker et al., Nucleic Acids Res. 20, 1691-1696 (1992)), transcription-based amplification (see D. Kwoh et al., Proc. Natl. Acad Sci. USA 86, 1173-1177 (1989)), self-sustained sequence replication (or "3SR") (see J. Guatelli et al., Proc. Natl. Acad. Sci. USA 87, 1874-1878 (1990)), the Qß replicase system (see P. Lizardi et al., BioTechnology 6, 1197-1202 (1988)), nucleic acid sequence-based amplification (or "NASBA") (see R. Lewis, Genetic Engineering News 12 (9), 1 (1992)), the repair chain reaction (or "RCR") (see R. Lewis, supra), and boomerang DNA amplification (or "BDA") (see R. Lewis, supra).

[0034] DNA amplification techniques such as the foregoing can involve the use of a probe, a pair of probes, or two pairs of probes which specifically bind to DNA containing the polymorphism of interest, but do not bind to DNA that does not contain the polymorphism of interest under the same hybridization conditions, and which serve as the primer or primers for the amplification of the DNA or a portion thereof in the amplification reaction. Such probes are sometimes referred to as amplification probes or primers herein.

[0035] In general, an oligonucleotide probe which is used to detect DNA containing a polymorphism of interest is an oligonucleotide probe which binds to DNA encoding that polymorphism, but does not bind to DNA that does not contain the polymorphism under the same hybridization conditions. The oligonucleotide probe is labelled with a suitable detectable group, such as those set forth below in connection with antibodies. Such probes are sometimes referred to as detection probes or primers herein.

[0036] Probes and primers, including those for either amplification and/or protection, are nucleotides (including naturally occurring nucleotides such as DNA and synthetic and/or modified nucleotides) are any suitable length, but are typically from 5, 6, or 8 nucleotides in length up to 40, 50 or 60 nucleotides in length, or more. Such probes and or primers may be immobilized on or coupled to a solid support such as a bead or chip in accordance with known techniques, and/or coupled to or labelled with a detectable group such as a fluorescent compound, a chemiluminescent compound, a radioactive element, or an enzyme in accordance with known techniques.

[0037] Polymerase chain reaction (PCR) may be carried out in accordance with known techniques. See, e.g., U.S. Pat. Nos. 4,683,195; 4,683,202; 4,800,159; and 4,965,188. In general, PCR involves, first, treating a nucleic acid sample (e.g., in the presence of a heat stable DNA polymerase) with one oligonucleotide primer for each strand of the specific sequence to be detected under hybridizing conditions so that an extension product of each primer is synthesized which is complementary to each nucleic acid strand, with the primers sufficiently complementary to each strand of the specific sequence to hybridize therewith so that the extension product synthesized from each primer, when it is separated from its complement, can serve as a template for synthesis of the extension product of the other primer, and then treating the sample under denaturing conditions to separate the primer extension products from their templates if the sequence or sequences to be detected are present. These steps are cyclically repeated until the desired degree of amplification is obtained. Detection of the amplified sequence may be carried out by adding to the reaction product an oligonucleotide probe capable of hybridizing to the reaction product (e.g., an

oligonucleotide probe of the present invention), the probe carrying a detectable label, and then detecting the label in accordance with known techniques, or by direct visualization on a gel. When PCR conditions allow for amplification of all ApoE allelic types, the types can be distinguished by hybridization with allelic specific probe, by restriction endonuclease digestion, by electrophoresis on denaturing gradient gels, or other techniques.

[0038] Ligase chain reaction (LCR) is also carried out in accordance with known techniques. See, e.g., R. Weiss, Science 254, 1292 (1991). In general, the reaction is carried out with two pairs of oligonucleotide probes: one pair binds to one strand of the sequence to be detected; the other pair binds to the other strand of the sequence to be detected. Each pair together completely overlaps the strand to which it corresponds. The reaction is carried out by, first, denaturing (e.g., separating) the strands of the sequence to be detected, then reacting the strands with the two pairs of oligonucleotide probes in the presence of a heat stable ligase so that each pair of oligonucleotide probes is ligated together, then separating the reaction product, and then cyclically repeating the process until the sequence has been amplified to the desired degree. Detection may then be carried out in like manner as described above with respect to PCR.

[0039] It will be readily appreciated that the detecting steps described herein may be carried out directly or indirectly. For example, a polymorphism could be detected by measuring by digestion with restriction enzymes, detection of polymorphic markers that are linked to the polymorphism, etc.

[0040] Kits useful for carrying out the methods of the present invention will, in general, comprise one or more oligonucleotide probes and other reagents for carrying out the methods as described above, such as restriction enzymes, optionally packaged with suitable instructions for carrying out the methods.

[0041] 2. Estrogen replacement therapy.

[0042] "Estrogen replacement therapy" as used herein (sometimes also referred to as "hormone replacement therapy" or HRT) refers to a long-term therapy in which estrogen or estrogenic active agents are administered to a subject continuously over an extended period of time (*e.g.*, one month, one year, or more) to maintain sustained blood levels of the active agent to combat the effects of menopause or hysterectomy (*e.g.*, loss of calcium from bone and increased incidience of classical osteoporotic fractures of the forearm and hip, ischemic heart disease, etc.). The administration may be daily or periodically.

[0043] Estrogen replacement therapy may be carried out by any suitable means. All typically involve administering an active agent such as estrogen or an estrogen analog (typically a steroid that has estrogen activity) to the subject in an estrogen replacement therapy effective amount, which is generally commensurate with an amount effective to enhance HDL levels as discussed above. Any suitable route of administration may be employed, including, but not limited to, oral administration, aerosol administration to airway surfaces, intravenous injection, subcutaneous injection, intramuscular injection, transdermal administration (*e.g.,* a patch), etc. Oral and transdermal formulations are currently preferred. Numerous estrogen replacement therapy preparations and protocols are known, including but not limited to those described in U.S. Patents Nos. 5,922,349; 5,897,539; 5,565,199; 5,468,736; 5,422,119; 5,288,717; and 5,023,084, the disclosures of all of which are incorporated by reference herein in their entirety. Other agents, such as progesterone (or progestin) in a hormone replacement therapy effective amount, may be administered along with the estrogen to provide a combination therapy, if desired (typically to reduce undesirable side-effects of estrogen monotherapy, as such estrogenic endometrial proliferation and corresponding risk of endometrial cancer).

[0044] Suitable active agents for estrogen replacement therapy include, but are not limited to, natural and synthetic estrogens such as conjugated equine estrogen, ethinyl estradiol, micronized estradiol, 17β estradiol, mestranol, estradiol valerate, 11-nitrato estradiol, 7-α-methyl-11-nitrato-estradiol, piperazine estrone sulfate, quinestranol, and 8,9-dehydroestereone (particularly alkali metal salts and sulfate esters thereof). *See, e.g.,* U.S. Patent No. 5,422,119 at column 6; U.S. Patent No. 5,288,717. Of course, all active agents may be prepared as a pharmaceutically acceptable salt or ester, in accordance with known techniques,

[0045] The progestin component may be any progestationally active compound, including but not limited to progsterone, 17-hydroxyprogesterone, dihydroprogesterone, medroxyprogesterone acetate, norethindrone, norethindrone acetate, norethynodrel, ethynodioldiacetate, norgesterel, levo-norgesterel, gestodene, delta-15-levonorgesterel, norgestimate, 17-deacetyl norgestimate, nomegestereol, nesterone, desogesterel and 3-keto-desogesteral. *See, e.g.,* U.S. Patent No. 5,422,119 at column 6.

[0046] In general, a pharmaceutical formulation or medicament for estrogen replacement therapy is prepared by bringing an effective amount of the active agent into contact with a pharmaceutically acceptable carrier, such as lactose or talc (for an oral

administration), intimately admixing the two, and forming (when necessary) the mixture into a suitable unit dosage form such as a patch for transdermal administration or a tablet, dragee, capsule or pill for an oral dosage form.

[0047] The amount of active agent administered will depend upon factors such as the specific active agent, the age, weight and condition of the subject, the route of administration, etc. For example, the estrogenic active agent may be administered in an a amount of from 0.3 to 1.2 mg daily for orally administered conjugated equine estrogen; or from about 25 μg/day to about 150 μg/day of transdermal β-estradiol.

[0048] Examples of commercially available estrogen preparations include: Alora™ (skin patch), Climara™ (skin patch), Estraderm™ (skin patch), FemPatch™ (skin patch), Estrace™ (pill or skin patch), Estrab™ (pill), Menset™ (pill), Ogen™ (pill), Ortho-est™ (pill), and Premarin™ (pill)

[0049] Examples of commercially available estrogen/progestin combination formulations include, but are not limited to, Combipatch™ (skin patch) and Prempro™ (pill).

[0050] The new polymorphisms described herein provide novel nucleic acids encoding the human estrogen receptor alpha, along with probes such as described above that bind selectively thereto. Such nucleic acids can be inserted into vectors such as plasmids, optionally associated with or placed under the control of a promoter, and the nucleic acids may be inserted into host cells and optionally expressed therein (when the promoter is operative in the host cell) to produce estrogen receptor alpha. The nucleic acids and the encoded proteins may be used in accordance with known techniques, such as described in US Patent No. 6,222,015 to H. Wilkinson.

[0051] The present invention also provides a method of conducting a clinical trial on a plurality of human female patients. Such methods advantageously permit the refinement of the patient population so that advantages of particular treatment regimens (typically administration of pharmaceutically active organic compound active agents) can be more accurately detected, particularly with respect to particular sub-populations of patients. In general, such methods comprise administering a test hormone replacement therapy to a plurality of subjects (a control or placebo therapy typically being administered to a separate but similarly characterized plurality of subjects) and detecting the presence of at least one estrogen receptor alpha polymorphism as described above in the plurality of subjects. The polymorphisms may be detected before, after, or concurrently with the step of administering the test therapy. The influence of detected polymorphism on the test therapy can then be

determined on any suitable parameter or potential treatment outcome or consequence, including but not limited to: *(i)* the efficacy of said hormone replacement therapy, *(ii)* a favorable response to said hormone replacement therapy with respect to cardiovascular health, *(iii)* a favorable response to said hormone replacement therapy with respect to risk of heart disease, and/or *(iv)* a favorable response to said hormone replacement with respect to HDL levels. Such determinations can be carried out in accordance with any suitable technique, including but not limited to those available from SAS, Inc., Cary, North Carolina, USA.

[0052] The present invention is explained in greater detail in the following non-limiting Examples.

[0053] EXAMPLE 1

[0054] In this example, we describe the association between several previously described and two newly identified sequence variants in the estrogen receptor-alpha gene and changes in HDL in response to treatment with estrogen replacement among women enrolled in the Estrogen Replacement and atherosclerosis (ERA) trial.

[0055] The ERA study population included 309 unrelated postmenopausal women with established coronary artery disease were enrolled at five clinical sites in the U.S. (Winston-Salem, Greensboro, and Charlotte, NC; Hartford, CT; and Birmingham, AL). Women with triglycerides >400 mg/dl, uncontrolled diabetes or hypertension, or excessive alcohol use were ineligible. Eligible women were randomized to receive daily oral estrogen (Premarin® 0.625 mg), estrogen plus progestin (medroxyprogesterone acetate [MPA]) 2.5 mg, or placebo and followed for an average of 3.2 years for progression of angiographically defined coronary disease. Plasma specimens obtained after overnight fasting were collected at baseline and annually thereafter for lipid and lipoprotein determinations. Buffy coats were separated from the baseline plasma specimens and frozen at -80°C for subsequent genetic analyses. Data on other potential confounders, including age, race, BMI, and physical activity were collected using standardized questionnaires and procedures. Herrington et al., *Control Clin Trials* 2000; 21:257-285.

[0056] Lipid and Hepatic Lipase Analyses

[0057] Fasting plasma specimens for lipoprotein determinations were obtained. Cholesterol and triglycerides were measured in the WFU Lipid Analytic Laboratory on a Technicon RA-1000 autoanalyzer as described in the Technicon technical manual for

cholesterol (SM4-0139A85) and for triglyceride (SM4-0189K87, glycerol phosphase-oxidase [GPO] blank method). The cholesterol method is based on the enzymatic cholesterol procedures of Allain et al., (*Clin Chem* 1974; 20:470), Roeschlau et al., (*Klin Chem Biochem* 1974; 12:226) and the Trinder peroxidase/4-aminophenazone system. *Ann Clin Biol Chem* 1969; 6:24-27. The triglycerides method was described by Fossati and Principe. *Clin Chem* 1982; 28:2077. Total glycerides in plasma were quantitated. HDL cholesterol was measured using the heparin-manganese precipitation procedure. *See*, Burstein et. al., *Clin Chem Acta* 1960; 5:609; and Lipid Clinics Research Program: *Manual of Clinic Operations; volume 1: Lipid and lipoprotein analysis*, Bethesda, MD, DHHS; 1982.. LDL cholesterol was calculated using the Friedewald formula. Lp(a) measurements were made on a COBAS FARA II centrifugal autoanalyzer.

[0058] Hepatic lipase was measured after subjects (who had fasted overnight) were given an intravenous bolus infusion of 60 units heparin per kg body weight. Fifteen minutes later, the post-heparin sample was drawn into tubes containing EDTA on ice, the plasma promptly separated, aprotinin added, and the sample rapidly frozen at -70°C. Lipase activity was assayed using [^{3}H]triolein-labeled Triton X-100 emulsion as described previously, with the addition of 1 mol/L NaCl.

[0059] DNA Isolation and Genotyping.

[0060] DNA was isolated from stored buffy coats using a standard guanidine thiocyanate procedure. Genotyping was performed for each single nucleotide polymorphism (SNP) using PCR followed by restriction enzyme digest (PCR-RFLP), allele-specific PCR (AS-PCR), or capillary electrophoresis (CE) on a 3700 DNA Analyzer (ABI, Inc., Foster City, CA). For the AS-PCR assays, a PCR reaction was performed with the external primer pair, followed by a second reaction with the allele-specific primer pair. PCR fragments from AS-PCR and PCR-RFLP assays were separated on 2% agarose gels and genotyped by the size of resulting fragments. For the CE assays, fluorescently labeled PCR fragments were diluted in water and run on 3700 DNA Analyzers. Genotypes were determined using Genotyper software (ABI, Inc.). SNPs located in coding regions are denoted using nucleotide number counted from the translation start site based on the Genebank reference sequence XM_045967.

[0061] DNA Sequencing and Analysis

[0062] In DNA from the 96 women with the highest or lowest HDL response to HRT, segments of the promoter region and the 5′ and 3′ regions of intervening sequence 1 (IVS1)

were PCR-amplified and sequenced using the ABI BigDye Terminator sequencing kit. Sequencing products were analyzed on an ABI 3700 DNA Analyzer. DNA sequencing data were aligned and analyzed using Sequencher DNA analysis software (Gene Codes Corp., Ann Arbor, MI).

[0063] Statistical Analyses

[0064] The χ^2 test was used to identify significant departures from Hardy-Weinberg equilibrium. Shuffling tests were performed to determine linkage disequilibrium between pairs of loci (Genetic Data Analysis, version 1.0215). Lipid and lipoprotein levels are presented as mean mean follow-up measurements obtained annually and at close-out. Generalized linear models were used to describe relationships among mean on-trial plasma lipids, estrogen treatment, and various genotypes after adjusting for: baseline lipid values and age; race (black, white, or other); diabetes (requiring medication); BMI (height [cm]/ weight^2 [kg]); smoking status at baseline (yes or no); physical activity (never, seldom [1-2 d/wk], sometimes [3-5 d/wk], often [5-7 d/wk]); and alcohol consumption (yes or no). Evidence for interaction was based on the nominal two-sided P-values from the F-test for the treatment by genotype interaction. For diallelic polymorphisms, P1 was used to indicate the less common, and P2 the more common, allele. Exploratory data analyses using additive, dominant, and recessive models revealed that carriers of the P2 allele for intron 1 polymorphisms (P1/P2 or P2/P2) responded similarly with respect to HDL and were therefore combined for some analyses. Effects of estrogen treatment were analyzed according to intention-to-treat, unless indicated otherwise. Exploratory data analyses revealed that the effect of genotype on lipid values during the trial was not different among women in the two active arms; therefore, these arms were collapsed unless otherwise indicated.

[0065] **Results**

[0066] **Figure 1** indicates the location of each polymorphism within the *ER*-α gene, including two novel SNPs in intron 1 (IVS1) identified as a result of resequencing. The nine SNPs and the TA repeat polymorphism were in Hardy-Weinberg equilibrium. Frequencies for the variant SNP alleles ranged from 7.3% to 47.8% (**Table 1**). The distribution of TA repeats in the promoter region microsatellite ranged from 18 to 34 (median = 26). The four SNPs in the 2 kb region 5′ of exon 2 were in linkage disequilibrium with each other and with the two SNPs in exon 1 ($P< 10^{-6}$) but not with SNPs located in intron 3, exon 4, or intron 5. The pattern of linkage disequilibrium was similar among white and black participants.

Table 1. Allele* and genotype frequencies (%) for each of the ER-α polymorphisms

Allele or genotype	+30 T→C** (exon 1)	+261 G→C (exon 1)	IVS1-1505 A→G	IVS1-1415 C→T	IVS1-401 T→C	IVS1-354 A→G	IVS3-17 T10→T9	+975 C→G (exon 4)	IVS5-33 T5→T4
	n = 290†	*n* = 289	*n* = 298	*n* = 301	*n* = 305	*n* = 305	*n* = 269	*n* = 301	*n* = 284
P1	47.8	7.3	43.6	30.7	45.2	34.3	38.1	26.1	8.3
P2	52.2	92.7	56.4	69.3	54.8	65.7	61.9	73.9	91.7
P1/P1	21.7	1.0	17.4	7.6	18.9	9.3	15.2	7.3	0.7
P1/P2	52.1	12.5	53.8	46.2	52.3	49.7	45.7	37.5	15.1
P2/P2	26.2	86.5	30.2	46.2	28.8	41.1	39.0	55.1	84.2

* P1 – less common allele, P2 - more common allele
** (P2→P1)
† n = number of women

Table 2. Baseline and Mean On-trial HDL levels* (mg/dl) according to treatment arm and four ER-α intron 1 genotypes

Genotype / Treatment	IVS1-1505		IVS1-1415		IVS1-401		IVS1-354	
	Baseline *Mean (SE)*	Follow-up *Mean (SE)*	Baseline *Mean (SE)*	Follow-up *Mean (SE)*	Baseline *Mean (SE)*	Follow-up *Mean (SE)*	Baseline *Mean (SE)*	Follow-up *Mean (SE)*
P1/P1								
HRT	48.9 (3.0)	60.7 (3.0)	45.0 (4.0)	59.4 (4.0)	47.4 (2.9)	60.4 (2.9)	45.1 (3.5)	59.8 (3.5)
Placebo	48.6 (3.3)	48.6 (3.4)	48.1 (4.7)	48.5 (5.0)	47.6 (3.1)	47.9 (3.2)	46.9 (4.3)	48.1 (4.5)
P1/P2								
HRT	46.2 (2.2)	52.6 (2.2)	48.5 (2.3)	55.1 (2.3)	47.2 (2.1)	53.1 (2.2)	48.3 (2.2)	54.6 (2.3)
Placebo	44.8 (2.6)	47.2 (2.7)	44.2 (2.7)	46.2 (2.8)	44.4 (2.6)	47.7 (2.6)	45.5 (2.6)	48.2 (2.6)
P2/P2								
HRT	44.8 (2.5)	50.2 (2.5)	45.1 (2.2)	51.4 (2.3)	42.8 (2.5)	48.8 (2.5)	44.9 (2.3)	51.1 (2.3)
Placebo	44.3 (3.0)	45.5 (3.2)	47.7 (2.6)	49.0 (2.7)	44.6 (3.0)	45.2 (3.1)	46.1 (2.8)	47.0 (2.8)
Interaction p-values								
Additive model**	0.0196		0.1975		0.0093		0.0507	
Dominant model+	0.0049		0.0739		0.0036		0.0175	

* After adjustment for age, race, BMI, diabetes, exercise, alcohol intake, and smoking
** (P1/P1 vs P1/P2 vs P2/P2) x treatment arm
\+ (P1/P1 vs P1/P2 and P2/P2) x treatment arm. In this model, P2 treated as a dominant allele

[0067] Increases in HDL level with HRT were greatest in women who were homozygous for the less common (P1) intron 1 alleles. P values for the HRT by genotype interactions using dominant models ranged from 0.0036 to 0.0739 (**Table 2**). When expressed as percent change from baseline, homozygotes for the less common intron 1 alleles experienced a 24% to 33% increase in HDL with HRT compared with a 13% increase in carriers of more common alleles. Baseline HDL levels were slightly higher in IVS1-401 C/C and IVS1-1505 G/G women compared with women with the IVS1-401 T/T and IVS1-1505 A/A genotypes, respectively (P = 0.052 and 0.063).

[0068] Among the four intron 1 SNPs, evidence for interaction was greatest for the IVS1-401 polymorphism (**Figure 2**). Women with the IVS1-401 C/C genotype who were assigned to HRT had a 13.1 mg/dl increase in HDL compared with a 6.0 mg/dl increase in women with the C/T or T/T genotypes (P value for HRT by IVS1-401 interaction = 0.0036). In analyses limited to women who took ≥ 80% of their study medication, the interaction was even more pronounced (P = 0.0004). Evidence of interaction was also present within each of the two randomly assigned active treatment arms (change in HDL by treatment and IVS1-401 status: estrogen, C/C 26.0%, C/T or T/T 14.9%; estrogen plus progestin, C/C 29.0%, C/T or T/T 11.1%; P for interaction = 0.029 and 0.007, respectively). When subjects were stratified into non-Hispanic whites (n = 221), African-Americans (n = 33), and others (n = 11), the pattern was preserved in all three groups, although only non-Hispanic whites were sufficiently numerous to support an inference of interaction with confidence (P = 0.023 for IVS1-401 C/C versus C/T or T/T).

[0069] In women on HRT with the IVS1-401 C/C genotype, HDL_3 increased by 13.6 mg/dl compared with 8.2 mg/dl in women with the C/T or T/T genotypes (P for interaction = 0.04) (**Figure 3**). In contrast, there was no effect of the IVS1-401 genotype on response of HDL_2 to HRT. HRT-associated increases in Apo-AI were also greatest for IVS1-401 C/C women (**Figure 3**); however, this increase was not significantly different than the increase observed in C/T or T/C women (36 mg/dl versus 28 mg/dl, P for interaction = 0.68). Similarly, the numerically greater reductions in LDL and ApoB among IVS1-401 C/C women were not sufficiently large to support an inference of interaction (data not shown). At the end of the trial, hepatic lipase levels were slightly lower in IVS1-401 C/C women compared to C/T or T/T women (P = 0.06). However, there was no evidence of interaction with HRT (change in hepatic lipase with HRT relative to placebo: C/C 1.4 mg/dl, C/T or T/T 2.0 mg/dl; P for interaction = 0.78). On the other hand, examination of another estrogen-

sensitive protein produced in the liver, sex hormone- binding globulin, also revealed a significant HRT by IVS1-401 interaction (P for interaction = 0.001) (**Figure 3**).

[0070] Despite the favorable effects on HDL levels, progression of angiographically defined coronary disease was not significantly different among women with the IVS1-401 C/C genotype on HRT compared to the other women assigned HRT; although, the power to detect such an interaction for the angiographic endpoint was extremely limited. None of the other *ER*-α polymorphisms examined, including several different classifications of the promoter TA repeat, was associated with change in HDL cholesterol in response to HRT.

[0071] Discussion

[0072] The estrogen receptor is a ligand-activated factor that augments gene transcription by binding to specific DNA response elements. The human estrogen receptor gene, located at 6q24.1, has been cloned, sequenced, and expressed in a variety of cell lines, and site-directed mutagenesis has identified domains which are highly conserved across species that are responsible for hormone or DNA binding and transcriptional activation. *See, e.g.* Ponglikitmongkol et al., *EMBO J* 1988; 7:3385-3388. Numerous naturally occurring sequence variants have also been identified, and their association with a variety of estrogen-dependent clinical phenotypes, including risk, age of onset, and estrogen-receptor status in breast cancer; spontaneous abortion, bone mineral density, body mass index, and hypertension have been examined.

[0073] A thymine-adenine (T-A) repeat has been identified in the genomic region 1174 bp 5′ of exon 1. Piva et al., *Biochem Biophys Res Commun* 1992;183:996-1002; and del Senno et al., *Hum Mol Genet* 1992;1:354. This microsatellite marker contains 10-27 T-A repeats that range in allelic frequency from <1% to 18%. Several investigators have also examined the relationship between ER polymorphisms and plasma lipids or atherosclerosis. Matsubara et al, in a study of 87 men and women, found no association between the XbaI or PvuII polymorphisms and plasma lipids or angiographically documented coronary disease. *Arterioscler Thromb Vasc Biol* 1997; 17:3006-3012. In another study, Kikuchi et al found that among 102 Japanese children aged 10 to 15 years, those homozygous for the XbaI polymorphism had significantly higher levels of LDL and apoB. *Acta Paediatr* 2000; 89:42-45. No association was evident with the PvuII polymorphism. In both studies, there was no apparent association with HDL levels, although the numbers of subjects were small and the analyses were not stratified by gender or estrogen use. In another study of 119 men undergoing coronary angiography, those with more severe disease or prior history of

myocardial infarction were more likely to have greater numbers of T-A repeats in the promoter region microsatellite marker. In contrast, in the current study both the XbaI and the PvuII polymorphisms and two novel polymorphisms, all in high degree of linkage disequilibrium with each other, were associated in varying degrees with baseline HDL level and even more dramatically with the response of HDL to estrogen treatment.

[0074] Only one previously published study has described the association between ER polymorphisms and estrogen-dependent phenomena among women taking estrogen replacement. In a study of 248 Korean women, Han et al determined XbaI and PvuII genotype and measured bone mineral density before and after one year of hormone replacement therapy. *Osteoporosis Int* 1999; 9:290-295. Although the differences were not statistically significant, the women who were homozygous for the XbaI or PvuII mutant alleles had higher BMD at baseline and less change over 1 year than women with one or two copies of the wild-type allele. Taken together, the data are consistent with the possibility that women with one of these polymorphisms are more responsive to endogenous or exogenous estrogen than other women.

[0075] It is not clear by what means the intron 1 polymorphisms are related to regulation of HDL levels. Hill et al. (*Cancer Res* 1989; 49:145-148) reported that the estrogen-receptor protein was less frequently expressed in breast cancer cells that were homozygous for the PvuII mutant allele; however, Yaich et al failed to find a similar relationship in a larger study of 257 cases of primary breast cancer. *Cancer Res* 1992; 52:77-83. Parl et al also found no correlation between the PvuII polymorphism and ER binding in breast cancer biopsy specimens. *Breast Cancer Treat Res* 1989; 14:57-64. Whether intron 1 polymorphisms could directly influence the transcription, splicing, stability, or function of the downstream products of the estrogen receptor gene, or be linked to other causative sequence variants in other locations, remains unknown. Likewise, the elements of HDL regulation that vary according to genotypes are not fully examined in this study. The significant increase in Apo A-I levels with estrogen treatment in those women with the favorable genotypes could be consistent with augmented Apo A-I synthesis through greater activation of the estrogen response element in the promoter region of this gene. However, elevated levels of HDL cholesterol are presumably due to greater downregulation of hepatic lipase and impaired removal of cholesterol ester from circulating HDL particles. Without more detailed studies of HDL kinetics, it is impossible to know if the augmented responses to estrogen treatment would produce a net benefit in terms of reverse cholesterol transport and pathogenesis of atherosclerosis.

[0076] **EXAMPLE 2**

[0077] **ESR1 Analysis**

[0078] TA repeat -1020 bp before exon 1

[0079] -1381 before the start codon

[0080] Novel SNPs:

[0081] A/G -1505 bp before exon 2

[0082] C/T -1415 bp before exon 2

[0083] Pvu II -401 bp before exon 2

[0084] Xba I -354 bp before exon 2

[0085] Regions sequenced:

[0086] -2246 to +53 bp around exon 2

[0087] currently sequencing –1324 bp to –259 bp before exon 1

[0088] +489-+1651 after exon 1

[0089] Estimated gaps:

[0090] E1

[0091] 34 kb

[0092] E2

[0093] Est 72 kb (?)

[0094] E3

[0095] ??

[0096] E4

[0097] ??

[0098] E5

[0099] 49 kb

[00100] E6

[00101] 33 kb

[00102] E7

[00103] 4.1 kb

[00104] E8

[00105] Primers for PCR:

[00106] 5' REGION OF EXON 1:

[00107] ESR1-PR1-F GCTTCAGCTACATTTGCATATTG (**SEQ ID NO: 4**)

[00108] ESR1-PR1-R ACCTCAGGTCACGAACCAAAG (**SEQ ID NO: 5**)

[00109] ESR1-PR2-F CCGAGAAGATCGAGTTGTAGGAC (**SEQ ID NO: 6**)

[00110] ESR1-PR2-R TCCTCGTTGGCTAGAAATACG (**SEQ ID NO: 7**)

[00111] REGION AROUND EXON 2:

[00112] ESR-3F GGTGGTGAAATGGAAAGAGATG (**SEQ ID NO: 8**)

[00113] ESR-3R ATATTGGCCCAGGACTTGGCAG (**SEQ ID NO: 9**)

[00114] ESR-4-2F CACAGGAACCTTCACTCCATC (**SEQ ID NO: 10**)

[00115] ESR-4-2R GCAGAGAAGTCCAACAAAGCA (**SEQ ID NO: 11**)

[00116] (ESR-4-2F and ESR-4-2R are the Primer pairs used to amplify the region containing the SNPs at –1415 and –1505 from the start of exon 2)

[00117] ESR-5F CATTGGTCTCTAATGGTTCTGAA (**SEQ ID NO: 12**)

[00118] ESR-5R TCTCCATGTTTCTACCAAAGATAC (**SEQ ID NO: 13**)

[00119] ER1 TCTTTCTCTGCCACCCTGGCGTCGATTATCTGA (**SEQ ID NO: 14**)

[00120] ER2 CTGCCACCCTATCTGTATCTTTTCCTATTCTCC (**SEQ ID NO: 15**)

[00121] REGION IN INTRON 1, 3' OF EXON1:

[00122] ESR-I1-1R TGGGCTGGCAGGAGATTA (**SEQ ID NO: 16**)

[00123] ESR-I1-1F GCTGCGTTCAGAGTCAARTTC (**SEQ ID NO: 17**)

[00124] ESR-I1-2R GGCTGAAGATGCACACTGAAT (**SEQ ID NO: 18**)

[00125] ESR-I1-2BF CTGGCATGTGACTTCTGACAG (**SEQ ID NO: 19**)

[00126] SEQUENCING PRIMERS:

[00127]	ESR2-SEQF	TGCCACCCTATCTGTATCTTTTC **(SEQ ID NO: 20)**
[00128]	ESR2-SEQMF1	ATCATAGCCTACTGCAGCCTC **(SEQ ID NO: 21)**
[00129]	ESR2-SEQMR1	AATTAGCTGAGAATGGTGATGTGT **(SEQ ID NO: 22)**
[00130]	ESR2-SEQMR2	ACAATTATTTCAGAACCATTA **(SEQ ID NO: 23)**
[00131]	ESR2-SEQR	CTTTCTCTGCCACCCTGGCGT **(SEQ ID NO: 24)**

[00132] **EXAMPLE 3**

[00133] **Intron 1**

[00134] Intron 1 of the estrogen receptor alpha gene is 34.2kb in size (**SEQ ID NO: 25**). The SNPs described herein reside in the last 1.6 kb of intron 1, before the start of Exon 2.

[00135] The foregoing is illustrative of the present invention, and is not to be construed as limiting thereof. The invention is defined by the following claims, with equivalents of the claims to be included therein.